



RECEIVED  
AUG 10 2001  
TECH CENTER 1600/2900

A-378CIP5.ST25.txt  
SEQUENCE LISTING

<110> BOYLE, WILLIAM J.  
LACEY, DAVID LEE  
CALZONE, FRANK J.  
CHANG, MING-SHI  
SENALDI, GIORGIO

<120> COMBINATION THERAPY FOR CONDITIONS LEADING TO BONE LOSS

<130> A-378CIP5

<140> US 09/613,591

<141> 2000-07-10

<150> US 09/457,647

<151> 1999-12-09

<150> US 09/350,670

<151> 1999-07-09

<150> US 08/706,945

<151> 1996-09-03

<150> US 08/577,788

<151> 1995-12-22

<160> 168

<170> PatentIn version 3.1

<210> 1

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Not I restriction site

<220>

<221> misc\_feature

<222> (28)..(35)

<223> N = any random nucleic acid

<400> 1

aaaggaagga aaaaagcggc cgctacannn nnnnnt

36

<210> 2

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Not I restriction site

<400> 2

tcgaccacg cgtccg

16

<210> 3

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Not I restriction site

<400> 3  
gggtgcgcag gc 12

<210> 4  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Not I restriction site

<400> 4  
tgtaaaacga cggccagt 18

<210> 5  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Not I restriction site

<400> 5  
caggaaacag ctatgac 18

<210> 6  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Not I restriction site

<400> 6  
caattaaccc tcactaaagg 20

<210> 7  
<211> 23  
<212> DNA  
<213> Rattus rattus

<400> 7  
gcattatgac ccagaaaccg gac 23

<210> 8  
<211> 23  
<212> DNA  
<213> Rattus rattus

<400> 8  
aggtagcgcc cttcctcaca ttc 23

<210> 9  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer

<400> 9

gactagtccc acaatgaaca agtggctgtg

30

<210> 10  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer

<400> 10  
ataagaatgc ggccgctaaa ctatgaaaca gcccagtgac cattc

45

<210> 11  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer

<400> 11  
gcctctagaa agagctggga c

21

<210> 12  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer

<400> 12  
cgccgtgttc catttatgag c

21

<210> 13  
<211> 24  
<212> DNA  
<213> Rattus rattus

<400> 13  
atcaaaggca gggcatactt cctg

24

<210> 14  
<211> 24  
<212> DNA  
<213> Rattus rattus

<400> 14  
gttgactcc tgtttcacgg tctg

24

<210> 15  
<211> 24  
<212> DNA  
<213> Rattus rattus

<400> 15  
caagacacct tgaaggcct gatg

24

<210> 16  
<211> 24

<212> DNA  
<213> Rattus rattus  
  
<400> 16  
taactttttac agaagagcat cagc 24  
  
<210> 17  
<211> 33  
<212> DNA  
<213> Rattus rattus  
  
<400> 17  
agcgcggccg catgaadaag tggctgtgct gcg 33  
  
<210> 18  
<211> 31  
<212> DNA  
<213> Rattus rattus  
  
<400> 18  
agctctagag aaacagccca gtgaccattc c 31  
  
<210> 19  
<211> 24  
<212> DNA  
<213> Rattus rattus  
  
<400> 19  
gtgaagctgt gcaagaacct gatg 24  
  
<210> 20  
<211> 24  
<212> DNA  
<213> Rattus rattus  
  
<400> 20  
atcaaaggca gggcatactt cctg 24  
  
<210> 21  
<211> 24  
<212> DNA  
<213> Homo sapiens  
  
<400> 21  
cagatcctga agctgctcag tttg 24  
  
<210> 22  
<211> 33  
<212> DNA  
<213> Homo sapiens  
  
<400> 22  
agcgcggccg cggggaccac aatgaacaag ttg 33  
  
<210> 23  
<211> 33  
<212> DNA  
<213> Homo sapiens  
  
<400> 23  
agctctagaa ttgtgaggaa acagctcaat ggc 33

<210> 24  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Not I restriction site  
  
 <400> 24  
 atagcggccg ctgagcccaa atcttgtgac aaaactcac 39  
  
 <210> 25  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Not I restriction site  
  
 <400> 25  
 tctagagtcg acttatcatt taccgggaga caggagagg ctctt 45  
  
 <210> 26  
 <211> 38  
 <212> DNA  
 <213> Mus musculus  
  
 <400> 26  
 cctctgagct caagcttccg aggaccacaa tgaacaag 38  
  
 <210> 27  
 <211> 43  
 <212> DNA  
 <213> Mus musculus  
  
 <400> 27  
 cctctgcccg cgctaagcag cttattttca cggattgaac ctg 43  
  
 <210> 28  
 <211> 38  
 <212> DNA  
 <213> Mus musculus  
  
 <400> 28  
 cctctgagct caagcttccg aggaccacaa tgaacaag 38  
  
 <210> 29  
 <211> 24  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 29  
 tccgtaagaa acagcccagt gacc 24  
  
 <210> 30  
 <211> 31  
 <212> DNA  
 <213> Mus musculus  
  
 <400> 30

cctctgcggc cgctgttgca tttcctttct g 31

<210> 31  
 <211> 19  
 <212> PRT  
 <213> Mus musculus

<400> 31

Glu Thr Leu Pro Pro Lys Tyr Leu His Tyr Asp Pro Glu Thr Gly His  
 1 5 10 15

Gln Leu Leu

<210> 32  
 <211> 21  
 <212> DNA  
 <213> Mus musculus

<400> 32

tcccttgccc tgaccactct t 21

<210> 33  
 <211> 34  
 <212> DNA  
 <213> Mus musculus

<400> 33

cctctgcggc cgcacacacg ttgtcatgtg ttgc 34

<210> 34  
 <211> 21  
 <212> DNA  
 <213> Mus musculus

<400> 34

tcccttgccc tgaccactct t 21

<210> 35  
 <211> 34  
 <212> DNA  
 <213> Mus musculus

<400> 35

cctctgcggc cgccttttgc gtggettctc tggt 34

<210> 36  
 <211> 37  
 <212> DNA  
 <213> Homo sapiens

<400> 36

cctctgagct caagcttggt ttccggggac cacaatg 37

<210> 37  
 <211> 38  
 <212> DNA  
 <213> Homo sapiens

<400> 37  
 cctctgcggc cgctaagcag cttattttta ctgaatgg 38

<210> 38  
 <211> 37  
 <212> DNA  
 <213> Homo sapiens

<400> 38  
 cctctgagct caagcttggg ttccggggac cacaatg 37

<210> 39  
 <211> 33  
 <212> DNA  
 <213> Homo sapiens

<400> 39  
 cctctgcggc cgccagggtg acatctattc cac 33

<210> 40  
 <211> 35  
 <212> DNA  
 <213> Mus musculus

<400> 40  
 ccgaagcttc caccatgaac aagtggctgt gctgc 35

<210> 41  
 <211> 40  
 <212> DNA  
 <213> Mus musculus

<400> 41  
 cctctgtcga ctattataag cagcttattt tcacggattg 40

<210> 42  
 <211> 21  
 <212> DNA  
 <213> Mus musculus

<400> 42  
 tcccttgccc tgaccactct t 21

<210> 43  
 <211> 35  
 <212> DNA  
 <213> Mus musculus

<400> 43  
 cctctgtcga cttaacacac gttgtcatgt gttgc 35

<210> 44  
 <211> 21  
 <212> DNA  
 <213> Mus musculus

<400> 44  
 tcccttgccc tgaccactct t 21

<210> 45

A-378CIP5.ST25.txt

<211> 35  
<212> DNA  
<213> Mus musculus

<400> 45  
cctctgtcga cttacttttg cgtggcttct ctgtt

35

<210> 46  
<211> 1548  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> pAMG21

<400> 46	
tgcacgcatt gcatacgtac cagaggggta cgctctcatc ccttgacggt ccgtagttta	60
ttttgctttc cgagtcagct ttctgacccg gaaagcaaaa tagacaacaa acagccactt	120
gcgagaggac tcatacctggt taggcggccc tcgcctaaac ttgcaacgct tcggtgccc	180
gcctcccacc gcccgctctg cgggcgggtat ttgacggtcc gtagtttaaat tcgtcttccg	240
gtaggactgc ctaccggaaa aacgcaaaga tgtttgagaa aacaaataaa aagatttatg	300
taagtttata cctgcagcat gaattgaaaa ttccataccc gttagttaac gaggacaatt	360
ttaacgaaat ctttatgaaa ccgtcgccaa acaacataac tcaaagtaaa cgcgtaacca	420
atttaccttt cactggcacg cgaatgatgt cggattataa aaactttata gggttctcga	480
aaaaggaagc gtacgggtgc gatttgtaag aaaaagagaa aaccaattta gcaacaaact	540
aaataataaa cgatataaat aaaaagctat taatagttga tctcttcctt gttaattacc	600
atacaagtat gtgcgtacat ttttatttga tagatatatc aacagaaaga gacttacacg	660
ttttgattcg taaggcttcg gtaataatcg tcatacttat ccctttgatt tgggtcacta	720
ttctggacta ctaaagcgaa gaaattaatg taaacctcta aaaaataaat gtcgtaacaa	780
aagtttatat aagggttaatt agccacttac taacctcaat cttattagat gatatcctag	840
tataaaataa tttaatcgca gtagtattat aacggaggta aaaaatccca ttaatagggtc	900
ttaactttat agtctaaatt ggtatcttac tcctatttac tagcgctcat ttattataag	960
tgttacatgg taaaatcagt atagtctatt cgtaactaat tatagtaata acgaagatgt	1020
ccgaaattaa aataattaat aagacattca cagcagccgt aaatacagaa agtatgggta	1080
gagaaatagg aatggataac aaacagcggt caaacgcac aatatatagt aattttgcca	1140
ttatctaact gttaaactaag attatttaac ctaaaaacag tgtgataata tagcgaactt	1200
tatgttaaca aattgtattc atggacatcc tagcatgtcc aatgcggtc ttttaccaaa	1260
caatatcagc taattagcta aactaagatc taaacaaaat tgattaattt cctccttatt	1320
gtataccaat tgcgcaacct taagctcgag tgatcacagc tggacgtccc atggtacctt	1380
cgaatgagct cctaggcgcc tttcttcttc ttcttcttct ttcgggcttt ccttcgactc	1440
aaccgacgac ggtggcgact cgttattgat cgtattgggg aaccccgag atttgccag	1500
aactcccaa aaaacgactt tcctccttgg cgagaagtgc gagaagtg	1548



```

<210> 47
<211> 48
<212> DNA
<213> Homo sapiens

<400> 47
ccggcggaca tttatcacac agcagctgat gagaagtttc ttcattcca 48

<210> 48
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> pAMG21

<400> 48
cgatttgatt ctagaaggag gaataacata tgggtaacgc gttggaattc ggtac 55

<210> 49
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> pAMG21

<400> 49
taaactaaga tcttcctcct tattgtatac caattgcgca accttaagc 49

<210> 50
<211> 1546
<212> DNA
<213> Artificial Sequence

<220>
<223> pAMG21

<220>
<221> misc_feature
<222> (1, 2, 1545 )..(1546)
<223> Unique AatII and SacII sticky ends

<400> 50
gcgtaacgta tgcattggtct ccccatgcga gagtagggaa ctgccaggca tcaaataaaa 60
cgaaaggctc agtcgaaaga ctgggccttt cgttttatct gttgtttgtc ggtgaacgct 120
ctcctgagta ggacaaatcc gccgggagcg gatttgaacg ttgcgaagca acggcccggg 180
gggtggcggg caggacgcc gccataaact gccaggcatc aaattaagca gaaggccatc 240
ctgacggatg gcctttttgc gtttctacaa actcttttgc ttatttttct aaatacatc 300
aaatatggac gtcgtactta acttttaag tatgggcaat caattgctcc tgttaaaatt 360
gcttagaaa tactttggca gcggtttgtt gtattgagtt tcatttgccg attggttaaa 420
tggaagtga ccgtgcgctt actacagcct aatatttttg aaatatccca agagcttttt 480
ccttcgcatg cccacgctaa acattctttt tctcttttgg ttaaatacgtt gtttgattta 540

```

## A-378CIP5.ST25.txt

```

ttatttgcta tatttatttt tcgataatta tcaactagag aaggaacaat taatgggatg 600
ttcatacacg catgtaaaaa taaactatct atatatgtgt ctttctctga atgtgcaaaa 660
ctaagcattc cgaagccatt attagcagta tgaataggga aactaaacc agtgataaga 720
cctgatgatt tcgcttcttt aattacattt ggagattttt tatttacagc attgttttca 780
aatatattcc aattaatcgg tgaatgattg gagttagaat aatctactat aggatcatat 840
tttattaaat tagcgtcatc ataatattgc ctccattttt tagggtaatt atccagaatt 900
gaaatatcag atttaaccat agaatgagga taaatgatcg cgagtaaata atattcacia 960
tgtaccattt tagtcatatc agataagcat tgattaatat cattattgct tctacaggct 1020
ttaattttat taattattct gtaagtgtcg tcggcattta tgtctttcat acccatctct 1080
ttatccttac ctattgtttg tcgcaagttt tgcgtgttat atatcattaa aacggtaata 1140
gattgacatt tgattctaata aaattggatt tttgtcacac tattatatcg cttgaaatac 1200
aattgtttta cataagtacc tgtaggatcg tacaggttta cgcaagaaaa tggtttggtta 1260
tagtcgatta atcgatttga ttctagattt gttttaacta attaaaggag gaataacata 1320
tggttaacgc gttggaattc gagctcacta gtgtcgacct gcagggtacc atggaagctt 1380
actcgaggat ccgcggaaag aagaagaaga agaagaaagc ccgaaaggaa gctgagttgg 1440
ctgctgccac cgctgagcaa taactagcat aacccttgg ggctctaaa cgggtcttga 1500
ggggtttttt gctgaaagga ggaaccgctc ttcacgctct tcacgc 1546

```

```

<210> 51
<211> 47
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> pAMG22

```

```

<400> 51
tatgaaacat catcaccatc accatcatgc tagcgttaac gcgttgg 47

```

```

<210> 52
<211> 49
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> pAMG22

```

```

<400> 52
actttgtagt agtggttagtg gtagtacgat cgcaattgcg caaccttaa 49

```

```

<210> 53
<211> 141
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> pAMG22

```

```

<400> 53

```

## A-378CIP5.ST25.txt

ctaattccgc tctcacctac caaacaatgc cccctgcaa aaaataaatt catataaaaa 60  
acatacagat aaccatctgc ggtgataaat tatctctggc ggtgttgaca taaataccac 120  
tggcggtgat actgagcaca t 141

<210> 54  
<211> 147  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> pAMG22

<400> 54  
tgcagattaa ggcgagagtg gatggtttgc tacgggggga cgttttttat ttaagtatat 60  
tttttgatg tctattgga gacgccacta tttaatagag accgccacaa ctgtatttat 120  
ggtgaccgcc actatgactc gtgtagc 147

<210> 55  
<211> 55  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> pAMG22

<400> 55  
cgatttgatt ctagaaggag gaataacata tggttaacgc gttggaattc ggtac 55

<210> 56  
<211> 49  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> pAMG22

<400> 56  
taaactaaga tcttctcct tattgtatac caattgcgca accttaagc 49

<210> 57  
<211> 668  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> pAMG22

<400> 57  
tgcacgcatt gcatacgtac cagaggggta cgctctcatc ccttgacggt ccgtagttta 60  
ttttgcttgc cgagtcagct ttctgacctg gaaagcaaaa tagacaacaa acagccactt 120  
gcgagaggac tcctctgtt tagggggccc tcgcctaaac ttgcaacgct tcgttgccgg 180  
gcctcccacc gcccgctctg cgggcggtat ttgacggtcc gtagtttaat tcgtcttccg 240  
gtaggactgc ctaccgaaa aacgcaaaga tgtttgagaa aacaaataaa aagatttatg 300  
taagtttata cctgcagagt attaaaaatt ttttaagtaa actgtttacg attttaagaa 360

A-378CIP5.ST25.txt

ctaattataa gagttaacac tcgcgagtgt taaatagcta aactaagatc taaactcaat	420
tgattaatfff cctccttatt gtataccaat tgcgcaacct taagctcgag tgatcacagc	480
tggacgtccc atgggtacct cgaatgagct cctaggcgcc tttctttctt ttctttcttct	540
ttcgggcttt ccttcgactc aaccgacgac ggtggcgact cgttattgat cgtattgggg	600
aaccccgag atttgcccag aactcccaa aaaacgactt tcctccttgg cgagaagtgc	660
gagaagtg	668

<210> 58  
 <211> 726  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> pAMG22

<400> 58	
gcgtaacgta tgcattggtct ccccatgcga gagtagggaa ctgccaggca tcaataaaaa	60
cgaagggtc agtcgaaaga ctgggccttt cgttttatct gttgtttgtc ggtgaacgct	120
ctcctgagta ggacaaatcc gccgggagcg gatttgaacg ttgcgaagca acggcccggg	180
gggtggcggg caggacgccc gccataaact gccaggcatc aaattaagca gaaggggcct	240
cccaccgccc gtcttgcggt cggtatttga cgggtccgtag tttaattcgt cttcgccatc	300
ctgacggatg gcctttttgc gtttctacaa actcttttgt ttatttttct aaatacatct	360
aaatatggac gtctcataat ttttaaaaaa ttcatttgac aaatgctaaa attcttgatt	420
aatattctca attgtgagcg ctccaaatct atcgatttga ttctagattt gttttaacta	480
attaaaggag gaataacata tgggttaacgc gttggaattc gagctcacta gtgtcgacct	540
gcagggtacc atggaagctt actcgaggat ccgcggaag aagaagaaga agaagaaagc	600
ccgaaaggaa gctgagttgg ctgctgccac cgctgagcaa taactagcat aacccttgg	660
ggcctctaaa cgggtcttga ggggtttttt gctgaaagga ggaaccgctc ttcacgctct	720
tcacgc	726

<210> 59  
 <211> 44  
 <212> DNA  
 <213> Homo sapiens

<400> 59	
tacgcactgg atccttataa gcagcttatt tttactgatt ggac	44

<210> 60  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens

<400> 60	
gtcctcctgg tacctaccta aaacaac	27

<210> 61

<211> 54  
 <212> DNA  
 <213> Homo sapiens

<400> 61  
 tatggatgaa gaaactttctc atcagctgct gtgtgataaa tgtccgccgg gtac 54

<210> 62  
 <211> 19  
 <212> PRT  
 <213> Homo sapiens

<400> 62  
 Met Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro  
 1 5 10 15

Gly Thr Tyr

<210> 63  
 <211> 84  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> pAMG21

<400> 63  
 tatggaaact tttcctccaa aatatcttca ttatgatgaa gaaactttctc atcagctgct 60  
 gtgtgataaa tgtccgccgg gtac 84

<210> 64  
 <211> 78  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> pAMG21

<400> 64  
 ccggcggaca tttatcacac agcagctgat gagaagtttc ttcatacataa tgaagatatt 60  
 ttggaggaaa agttttcca 78

<210> 65  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> pAMG21-MuOPG

<400> 65  
 tacgcactgg atccttataa gcagcttatt ttcacggatt gaac 44

<210> 66  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> pAMG21-MuOPG  
  
 <400> 66  
 gtgctcctgg tacctaccta aaacagcact gcacagtg 38  
  
 <210> 67  
 <211> 84  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> pAMG21-MuOPG  
  
 <400> 67  
 tatggaaact ctgcctccaa aatacctgca ttacgatccg gaaactggtc atcagctgct 60  
 gtgtgataaa tgtgctccgg gtac 84  
  
 <210> 68  
 <211> 78  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> pAMG21-MuOPG  
  
 <400> 68  
 ccggagcaca tttatcacac agcagctgat gaccagtttc cggatcgtaa tgcaggtatt 60  
 ttggaggcag agttttcca 78  
  
 <210> 69  
 <211> 54  
 <212> DNA  
 <213> Mus musculus  
  
 <400> 69  
 tatggacca gaaactggtc atcagctgct gtgtgataaa tgtgctccgg gtac 54  
  
 <210> 70  
 <211> 48  
 <212> DNA  
 <213> Mus musculus  
  
 <400> 70  
 ccggagcaca tttatcacac agcagctgat gaccagtttc tgggtcca 48  
  
 <210> 71  
 <211> 87  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> pAMG21  
  
 <400> 71  
 tatgaaagaa actctgcctc caaaatacct gcattacgat ccggaaactg gtcatcagct 60  
 gctgtgtgat aaatgtgctc cgggtac 87  
  
 <210> 72

<211> 81  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> pAMG21  
  
 <400> 72  
 ccggagcaca tttatcacac agcagctgat gaccagtttc cggatcgtaa tgcaggtatt 60  
 ttggaggcag agtttctttc a 81  
  
 <210> 73  
 <211> 71  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> pAMG21  
  
 <400> 73  
 gttctcctca tatgaaacat catcaccatc accatcatga aactctgcct ccaaataacc 60  
 tgcattacga t 71  
  
 <210> 74  
 <211> 43  
 <212> DNA  
 <213> Mus musculus  
  
 <400> 74  
 gttctcctca tatgaaagaa actctgcctc caaaatacct gca 43  
  
 <210> 75  
 <211> 76  
 <212> DNA  
 <213> Mus musculus  
  
 <400> 75  
 tacgcactgg atccttaatg atggtgatgg tgatgatgta agcagcttat tttcacggat 60  
 tgaacctgat tcccta 76  
  
 <210> 76  
 <211> 47  
 <212> DNA  
 <213> Mus musculus  
  
 <400> 76  
 gttctcctca tatgaaatac ctgcattacg atccggaaac tggatcat 47  
  
 <210> 77  
 <211> 43  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 77  
 gttctcctat taatgaaata tcttcattat gatgaagaaa ctt 43  
  
 <210> 78  
 <211> 40  
 <212> DNA

<213> Homo sapiens  
 <400> 78  
 tacgcactgg atccttataa gcagcttatt tttactgatt 40  
  
 <210> 79  
 <211> 40  
 <212> DNA  
 <213> Mus musculus  
  
 <400> 79  
 gttctcctca tatggaaact ctgcctccaa aatacctgca 40  
  
 <210> 80  
 <211> 43  
 <212> DNA  
 <213> Mus musculus  
  
 <400> 80  
 tacgcactgg atccttatgt tgcatttcct ttctgaatta gca 43  
  
 <210> 81  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> pAMG21  
  
 <400> 81  
 ccggaaacag ataatgag 18  
  
 <210> 82  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> pAMG21  
  
 <400> 82  
 gatcctcatt atctgttt 18  
  
 <210> 83  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> pAMG21  
  
 <400> 83  
 ccggaaacag agaagccacg caaaagtaag 30  
  
 <210> 84  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> pAMG21



<400> 84  
 gatccttact tttgcgtggc ttctctgttt 30

<210> 85  
 <211> 12  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> pAMG21

<400> 85  
 tatgttaatg ag 12

<210> 86  
 <211> 14  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> pAMG21

<400> 86  
 gatcctcatt aaca 14

<210> 87  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> pAMG21

<400> 87  
 tatgttccgg aaacagttaa g 21

<210> 88  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> pAMG21

<400> 88  
 gatccttaac tgtttccgga aca 23

<210> 89  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> pAMG21

<400> 89  
 tatgttccgg aaacagtgaa tcaactcaaa aataag 36

<210> 90  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> pAMG21  
  
 <400> 90  
 gatccttatt tttgagttga ttcactgttt ccggaaca 38  
  
 <210> 91  
 <211> 100  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> pAMG21  
  
 <400> 91  
 ctagcgacga cgacgacaaa gaaactctgc ctccaaaata cctgcattac gatccggaaa 60  
 ctgggtcatca gctgctgtgt cataaatgtg ctccgggtac 100  
  
 <210> 92  
 <211> 92  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> pAMG21  
  
 <400> 92  
 ccggagcaca tttatcacac agcagctgat gaccagtttc cggatcgtaa tgcaggtatt 60  
 ttggaggcag agttttctttg tcgtcgtcgt cg 92  
  
 <210> 93  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> pAMG21-huOPG  
  
 <400> 93  
 acaaacacaa tcgatttgat actaga 26  
  
 <210> 94  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> pAMG21-huOPG  
  
 <400> 94  
 tttgttttaa ctaattaaag gaggaataaa atatgagagg atcgcatcac 50  
  
 <210> 95  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> pAMG21-huOPG

<400> 95  
 catcaccatc acgaaacctt cccgccgaaa tacctgcact acgacgaaga 50

<210> 96  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> pAMG21-huOPG

<400> 96  
 aacctccac cagctgctgt gcgacaaatg cccgccgggt acccaaaca 49

<210> 97  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> pAMG21-huOPG

<400> 97  
 tgtttgggta cccggcgggc atttgt 26

<210> 98  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> pAMG21-huOPG

<400> 98  
 cgcacagcag ctggtgggag gtttcttcgt cgtagtgcag gtatttcggc 50

<210> 99  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> pAMG21-huOPG

<400> 99  
 gggaaggttt cgtgatggtg atggtgatgc catcctctca tattttatt 49

<210> 100  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> pAMG21-huOPG

<400> 100  
 cctcctttaa ttagttaaaa caaatctagt atcaaacga ttgtgtttgt 50

<210> 101  
 <211> 59  
 <212> DNA  
 <213> Homo sapiens

<400> 101  
 acaaacacaa tcgatttgat actagatttg ttttaactaa ttaaaggagg aataaaatg 59

<210> 102  
 <211> 48  
 <212> DNA  
 <213> Homo sapiens

<400> 102  
 ctaattaaag gaggaataaa atgaaagaaa cttttcctcc aaaatatc 48

<210> 103  
 <211> 31  
 <212> DNA  
 <213> Homo sapiens

<400> 103  
 tgtttgggta cccggcggac atttatcaca c 31

<210> 104  
 <211> 59  
 <212> DNA  
 <213> Homo sapiens

<400> 104  
 acaaacacaa tcgatttgat actagatttg ttttaactaa ttaaaggagg aataaaatg 59

<210> 105  
 <211> 54  
 <212> DNA  
 <213> Homo sapiens

<400> 105  
 ctaattaaag gaggaataaa atgaaaaaaa aagaaacttt tcctccaaaa tadc 54

<210> 106  
 <211> 31  
 <212> DNA  
 <213> Homo sapiens

<400> 106  
 tgtttgggta cccggcggac atttatcaca c 31

<210> 107  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer for FchOPG fusion protein.

<400> 107  
 cagcccgggt aaaatggaaa cgtttcctcc aaaatatctt catt 44

<210> 108  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>

A-378CIP5.ST25.txt  
<223> PCR primer for FchOPG fusion protein.

<400> 108  
cgtttccatt ttacccgggc tgagcgagag gctcttctgc gtgt 44

<210> 109  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Fc/muOPG

<400> 109  
cgctcagccc gggtaaaatg gaaacggtgc ctccaaaata cctgc 45

<210> 110  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Fc/muOPG

<400> 110  
ccattttacc cgggctgagc gagaggctct tctgcgtgt 39

<210> 111  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> muOPG

<400> 111  
gaaaataaga tgcttagctg cagctgaacc aaaatc 36

<210> 112  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> muOPG

<400> 112  
cagctgcagc taagcagctt attttcacgg attg 34

<210> 113  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> huOPG

<400> 113  
aaaaataagc tgcttagctg cagctgaacc aaaatc 36

<210> 114  
<211> 35

```

<212> DNA
<213> Artificial Sequence

<220>
<223> huOPG

<400> 114
cagctgcagc taagcagctt atttttactg attgg 35

<210> 115
<211> 102
<212> DNA
<213> Artificial Sequence

<220>
<223> pAMG21-huOPG

<220>
<221> misc_feature
<223> Linker with XbaI and KpnI sites inserted into human sequence.

<400> 115
ctagaaggag gaataacata tggaaacttt tgctccaaaa tatcttcatt atgatgaaga 60
aactagtcac cagctgctgt gtgataaatg tccgccgggt ac 102

<210> 116
<211> 94
<212> DNA
<213> Artificial

<400> 116
ccggcggaca tttatcacac agcagctgat gactagtttc ttcatacataa tgaagatatt 60
ttggagcaaa agtttccata tgttattcct cctt 94

<210> 117
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> huOPG

<400> 117
ctagaaggag gaataacata tggaaacttt tcctgctaaa tatcttcatt atgatgaaga 60
aa 62

<210> 118
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> huOPG

<400> 118
ctagtttctt catcataatg aagatattta gcaggaaaag tttccatatg ttattcctcc 60
tt 62

```

A-378CIP5.ST25.txt

<210> 119  
 <211> 51  
 <212> PRT  
 <213> Homo sapiens

<400> 119

Tyr His Tyr Tyr Asp Gln Asn Gly Arg Met Cys Glu Glu Cys His Met  
 1 5 10 15

Cys Gln Pro Gly His Phe Leu Val Lys His Cys Lys Gln Pro Lys Arg  
 20 25 30

Asp Thr Val Cys His Lys Pro Cys Glu Pro Gly Val Thr Tyr Thr Asp  
 35 40 45

Asp Trp His  
 50

<210> 120  
 <211> 2432  
 <212> DNA  
 <213> Rattus rattus

<220>  
 <221> CDS  
 <222> (124)..(1326)  
 <223>

<400> 120  
 atcaaaggca gggcatactt cctgttgccc agaccttata taaaacgtca tgttcgacctg 60  
 ggcagcagag aagcacctag cactggccca gcggtgccc cctgaggttt ccagaggacc 120  
 aca atg aac aag tgg ctg tgc tgt gca ctc ctg gtg ttc ttg gac atc 168  
 Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile  
 1 5 10 15  
 att gaa tgg aca acc cag gaa acc ttt cct cca aaa tac ttg cat tat 216  
 Ile Glu Trp Thr Thr Gln Glu Thr Phe Pro Lys Tyr Leu His Tyr  
 20 25 30  
 gac cca gaa acc gga cgt cag ctc ttg tgt gac aaa tgt gct cct ggc 264  
 Asp Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly  
 35 40 45  
 acc tac cta aaa cag cac tgc aca gtc agg agg aag aca ctg tgt gtc 312  
 Thr Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val  
 50 55 60  
 cct tgc cct gac tac tct tat aca gac agc tgg cac acg agt gat gaa 360  
 Pro Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu  
 65 70 75  
 tgc gtg tac tgc agc ccc gtg tgc aag gaa ctg cag acc gtg aaa cag 408  
 Cys Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln  
 80 85 90 95  
 gag tgc aac cgc acc cac aac cga gtg tgc gaa tgt gag gaa ggg cgc 456  
 Glu Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg  
 100 105 110  
 tac ctg gag ctc gaa ttc tgc ttg aag cac cgg agc tgt ccc cca ggc 504

## A-378CIP5.ST25.txt

Tyr	Leu	Glu	Leu	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	
			115					120					125			
ttg	ggt	gtg	ctg	cag	gct	ggg	acc	cca	gag	cga	aac	acg	ggt	tgc	aaa	552
Leu	Gly	Val	Leu	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	
		130					135					140				
aga	tgt	ccg	gat	ggg	ttc	ttc	tca	ggt	gag	acg	tca	tcg	aaa	gca	ccc	600
Arg	Cys	Pro	Asp	Gly	Phe	Phe	Ser	Gly	Glu	Thr	Ser	Ser	Lys	Ala	Pro	
	145					150					155					
tgt	agg	aaa	cac	acc	aac	tgc	agc	tca	ctt	ggc	ctc	ctg	cta	att	cag	648
Cys	Arg	Lys	His	Thr	Asn	Cys	Ser	Ser	Leu	Gly	Leu	Leu	Leu	Ile	Gln	
160					165					170					175	
aaa	gga	aat	gca	aca	cat	gac	aat	gta	tgt	tcc	gga	aac	aga	gaa	gca	696
Lys	Gly	Asn	Ala	Thr	His	Asp	Asn	Val	Cys	Ser	Gly	Asn	Arg	Glu	Ala	
				180					185					190		
act	caa	aat	tgt	gaa	ata	gat	gtc	acc	ctg	tgc	gaa	gag	gca	ttc	ttc	744
Thr	Gln	Asn	Cys	Glu	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	
			195					200					205			
agg	ttt	gct	gtg	cct	acc	aag	att	ata	ccg	aat	tgg	ctg	agt	ggt	ctg	792
Arg	Phe	Ala	Val	Pro	Thr	Lys	Ile	Ile	Pro	Asn	Trp	Leu	Ser	Val	Leu	
		210					215					220				
gtg	gac	agt	ttg	cct	ggg	acc	aaa	gtg	aat	gca	gag	agt	gta	gag	agg	840
Val	Asp	Ser	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	
	225					230					235					
ata	aaa	cgg	aga	cac	agc	tcg	caa	gag	caa	act	ttc	cag	cta	ctt	aag	888
Ile	Lys	Arg	Arg	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	
240					245					250					255	
ctg	tgg	aag	cat	caa	aac	aga	gac	cag	gaa	atg	gtg	aag	aag	atc	atc	936
Leu	Trp	Lys	His	Gln	Asn	Arg	Asp	Gln	Glu	Met	Val	Lys	Lys	Ile	Ile	
				260					265					270		
caa	gac	att	gac	ctc	tgt	gaa	agc	agt	gtg	caa	cgg	cat	atc	ggc	cac	984
Gln	Asp	Ile	Asp	Leu	Cys	Glu	Ser	Ser	Val	Gln	Arg	His	Ile	Gly	His	
			275					280					285			
gcg	aac	ctc	acc	aca	gag	cag	ctc	cgc	atc	ttg	atg	gag	agc	ttg	cct	1032
Ala	Asn	Leu	Thr	Thr	Glu	Gln	Leu	Arg	Ile	Leu	Met	Glu	Ser	Leu	Pro	
		290					295					300				
ggg	aag	aag	atc	agc	cca	gac	gag	att	gag	aga	acg	aga	aag	acc	tgc	1080
Gly	Lys	Lys	Ile	Ser	Pro	Asp	Glu	Ile	Glu	Arg	Thr	Arg	Lys	Thr	Cys	
	305					310					315					
aaa	ccc	agc	gag	cag	ctc	ctg	aag	cta	ctg	agc	ttg	tgg	agg	atc	aaa	1128
Lys	Pro	Ser	Glu	Gln	Leu	Leu	Lys	Leu	Leu	Ser	Leu	Trp	Arg	Ile	Lys	
320					325					330					335	
aat	gga	gac	caa	gac	acc	ttg	aag	ggc	ctg	atg	tac	gca	ctc	aag	cac	1176
Asn	Gly	Asp	Gln	Asp	Thr	Leu	Lys	Gly	Leu	Met	Tyr	Ala	Leu	Lys	His	
				340					345					350		
ttg	aaa	gca	tac	cac	ttt	ccc	aaa	acc	gtc	acc	cac	agt	ctg	agg	aag	1224
Leu	Lys	Ala	Tyr	His	Phe	Pro	Lys	Thr	Val	Thr	His	Ser	Leu	Arg	Lys	
			355					360					365			
acc	atc	agg	ttc	ttg	cac	agc	ttc	acc	atg	tac	cga	ttg	tat	cag	aaa	1272
Thr	Ile	Arg	Phe	Leu	His	Ser	Phe	Thr	Met	Tyr	Arg	Leu	Tyr	Gln	Lys	
		370					375					380				
ctc	ttt	cta	gaa	atg	ata	ggg	aat	cag	gtt	caa	tca	gtg	aag	ata	agc	1320



## A-378CIP5.ST25.txt

Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser  
 385 390 395

tgc tta tagttaggaa tggtcactgg gctgtttctt caggatgggc caacactgat 1376  
 Cys Leu  
 400

ggagcagatg gctgcttctc cggctcttga aatggcagtt gattcctttc tcatcagttg 1436  
 gtgggaatga agatcctcca gcccaacaca cacactgggg agtctgagtc aggagagtga 1496  
 ggcaggctat ttgataattg tgcaaagctg ccagggtgtac acctagaaag tcaagcacc 1556  
 tgagaaagag gatattttta taacctcaaa cataggccct ttccttctc tccttatgga 1616  
 tgagtactca gaaggcttct actatcttct gtgtcatccc tagatgaagg cctcttttat 1676  
 ttattttttt attctttttt tcggagctgg ggaccgaacc cagggccttg cgcttgcgag 1736  
 gcaagtgtc taccactgag ctaaactctc aaccctgaa ggctctttc tttctgctc 1796  
 tgatagtcta tgacattctt ttttctacaa ttcgtatcag gtgcacgagc cttatcccat 1856  
 ttgtaggttt ctaggcaagt tgaccgttag ctatttttcc ctctgaagat ttgattcgag 1916  
 ttgcagactt ggctagacaa gcaggggtag gttatggtag tttatttaac agactgccac 1976  
 caggagtcca gtgtttcttg ttcctctgta gttgtaccta agctgactcc aagtacattt 2036  
 agtatgaaaa ataactcaaa aattttattc cttctatcaa cattggctag ctttggttca 2096  
 gggcactaaa agaaactact atatggagaa agaattgata ttgccccaa cgttcaacaa 2156  
 cccaatagtt tatccagctg tcatgcctgg ttcagtgtct actgactatg cgccctctta 2216  
 ttactgcatg cagtaattca actggaaata gtaataataa taatagaaat aaaatctaga 2276  
 ctccattgga tctctctgaa tatgggaata tctaacttaa gaagctttga gatttcagtt 2336  
 gtgttaaagg cttttattaa aaagctgatg ctcttctgta aaagttacta atatatctgt 2396  
 aagactatta cagtattgct atttatatcc atccag 2432

<210> 121  
 <211> 401  
 <212> PRT  
 <213> Rattus rattus

<400> 121

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile Ile  
 1 5 10 15

Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 20 25 30

Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr  
 35 40 45

Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro  
 50 55 60

Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
 Page 25

65

70

75

80

Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln Glu  
85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr  
100 105 110

Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Leu  
115 120 125

Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
130 135 140

Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys  
145 150 155 160

Arg Lys His Thr Asn Cys Ser Ser Leu Gly Leu Leu Leu Ile Gln Lys  
165 170 175

Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr  
180 185 190

Gln Asn Cys Glu Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
195 200 205

Phe Ala Val Pro Thr Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val  
210 215 220

Asp Ser Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
225 230 235 240

Lys Arg Arg His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
245 250 255

Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln  
260 265 270

Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Ile Gly His Ala  
275 280 285

Asn Leu Thr Thr Glu Gln Leu Arg Ile Leu Met Glu Ser Leu Pro Gly  
290 295 300

Lys Lys Ile Ser Pro Asp Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys  
305 310 315 320

Pro Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
325 330 335

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu  
Page 26

340

345

350

Lys Ala Tyr His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr  
 355 360 365

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu  
 370 375 380

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
 385 390 395 400

Leu

<210> 122  
 <211> 1325  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (91)..(1293)  
 <223>

<220>  
 <221> misc\_feature  
 <222> (11)..(11)  
 <223> At position 11, R is a purine.

<400> 122  
 ccttatataa racgtcatga ttgcctgggc tgcagagacg cacctagcac tgaccagcg 60  
 gctgcctcct gaggtttccc gaggaccaca atg aac aag tgg ctg tgc tgc gca 114  
 Met Asn Lys Trp Leu Cys Cys Ala  
 1 5  
 ctc ctg gtg ctc ctg gac atc att gaa tgg aca acc cag gaa acc ctt 162  
 Leu Leu Val Leu Leu Asp Ile Ile Glu Trp Thr Thr Gln Glu Thr Leu  
 10 15 20  
 ctt cca aag tac ttg cat tat gac cca gaa act ggt cat cag ctc ctg 210  
 Leu Pro Lys Tyr Leu His Tyr Asp Pro Glu Thr Gly His Gln Leu Leu  
 25 30 35 40  
 tgt gac aaa tgt gct cct ggc acc tac cta aaa cag cac tgc aca gtg 258  
 Cys Asp Lys Cys Ala Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Val  
 45 50 55  
 agg agg aag aca ttg tgt gtc cct tgc cct gac cac tct tat acg gac 306  
 Arg Arg Lys Thr Leu Cys Val Pro Cys Pro Asp His Ser Tyr Thr Asp  
 60 65 70  
 agc tgg cac acc agt gat gag tgt gtg tat tgc agc cca gtg tgc aag 354  
 Ser Trp His Thr Ser Asp Glu Cys Val Tyr Cys Ser Pro Val Cys Lys  
 75 80 85  
 gaa ctg cag tcc gtg aag cag gag tgc aac cgc acc cac aac cga gtg 402  
 Glu Leu Gln Ser Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val  
 90 95 100  
 tgt gag tgt gag gaa ggg cgt tac ctg gag atc gaa ttc tgc ttg aag 450

## A-378CIP5.ST25.txt

Cys 105	Glu	Cys	Glu	Glu	Gly 110	Arg	Tyr	Leu	Glu	Ile 115	Glu	Phe	Cys	Leu	Lys 120	
cac	cg	ag	tgt	ccc	ccg	ggc	tcc	ggc	gtg	gtg	caa	gct	gga	acc	cca	498
His	Arg	Ser	Cys	Pro 125	Pro	Gly	Ser	Gly	Val 130	Val	Gln	Ala	Gly	Thr 135	Pro	
gag	cga	aac	aca	gtt	tgc	aaa	aaa	tgt	cca	gat	ggg	ttc	ttc	tca	ggt	546
Glu	Arg	Asn	Thr 140	Val	Cys	Lys	Lys	Cys 145	Pro	Asp	Gly	Phe	Phe 150	Ser	Gly	
gag	act	tca	tcg	aaa	gca	ccc	tgt	ata	aaa	cac	acg	aac	tgc	agc	aca	594
Glu	Thr	Ser 155	Ser	Lys	Ala	Pro	Cys 160	Ile	Lys	His	Thr	Asn 165	Cys	Ser	Thr	
ttt	ggc	ctc	ctg	cta	att	cag	aaa	gga	aat	gca	aca	cat	gac	aac	tgt	642
Phe	Gly 170	Leu	Leu	Leu	Ile	Gln 175	Lys	Gly	Asn	Ala	Thr 180	His	Asp	Asn	Cys	
tgt	tcc	gga	aac	aga	gaa	gcc	acg	caa	aag	tgt	gga	ata	gat	gtc	acc	690
Cys 185	Ser	Gly	Asn	Arg	Glu 190	Ala	Thr	Gln	Lys	Cys 195	Gly	Ile	Asp	Val 200	Thr	
ctg	tgt	gaa	gag	gcc	ttc	ttc	agg	ttt	gct	gtt	cct	acc	aag	att	ata	738
Leu	Cys	Glu	Glu	Ala 205	Phe	Phe	Arg	Phe	Ala 210	Val	Pro	Thr	Lys	Ile 215	Ile	
cca	aat	tgg	ctg	agt	gtt	ttg	gtg	gac	agt	ttg	cct	ggg	acc	aaa	gtg	786
Pro	Asn	Trp 220	Leu	Ser	Val	Leu	Val	Asp 225	Ser	Leu	Pro	Gly	Thr 230	Lys	Val	
aat	gcc	gag	agt	gta	gag	agg	ata	aaa	cgg	aga	cac	agc	tca	caa	gag	834
Asn	Ala	Glu 235	Ser	Val	Glu	Arg	Ile 240	Lys	Arg	Arg	His	Ser 245	Ser	Gln	Glu	
caa	acc	ttc	cag	ctg	ctg	aag	ctg	tgg	aaa	cat	caa	aac	aga	gac	cag	882
Gln	Thr 250	Phe	Gln	Leu	Leu	Lys 255	Leu	Trp	Lys	His	Gln 260	Asn	Arg	Asp	Gln	
gaa	atg	gtg	aag	aag	atc	atc	caa	gac	att	gac	ctc	tgt	gaa	agc	agc	930
Glu 265	Met	Val	Lys	Lys	Ile 270	Ile	Gln	Asp	Ile	Asp 275	Leu	Cys	Glu	Ser	Ser 280	
gtg	cag	cg	cat	ctc	ggc	cac	tcg	aac	ctc	acc	aca	gag	cag	ctt	ctt	978
Val	Gln	Arg	His 285	Leu	Gly	His	Ser	Asn 290	Leu	Thr	Thr	Glu	Gln 295	Leu	Leu	
gcc	ttg	atg	gag	agc	ctg	cct	ggg	aag	aag	atc	agc	cca	gaa	gag	att	1026
Ala	Leu	Met	Glu 300	Ser	Leu	Pro	Gly	Lys 305	Lys	Ile	Ser	Pro	Glu 310	Glu	Ile	
gag	aga	acg	aga	aag	acc	tgc	aaa	tcg	agc	gag	cag	ctc	ctg	aag	cta	1074
Glu	Arg	Thr 315	Arg	Lys	Thr	Cys	Lys 320	Ser	Ser	Glu	Gln	Leu 325	Leu	Lys	Leu	
ctc	agt	tta	tgg	agg	atc	aaa	aat	ggg	gac	caa	gac	acc	ttg	aag	ggc	1122
Leu	Ser 330	Leu	Trp	Arg	Ile	Lys 335	Asn	Gly	Asp	Gln 340	Asp	Thr	Leu	Lys	Gly	
ctg	atg	tat	gcc	ctc	aag	cac	ttg	aaa	aca	tcc	cac	ttt	ccc	aaa	act	1170
Leu	Met	Tyr	Ala	Leu	Lys 350	His	Leu	Lys	Thr	Ser 355	His	Phe	Pro	Lys	Thr 360	
gtc	acc	cac	agt	ctg	agg	aag	acc	atg	agg	ttc	ctg	cac	agc	ttc	aca	1218
Val	Thr	His	Ser 365	Leu	Arg	Lys	Thr	Met	Arg 370	Phe	Leu	His	Ser	Phe 375	Thr	
atg	tac	aga	ctg	tat	cag	aag	ctc	ttt	tta	gaa	atg	ata	ggg	aat	cag	1266

## A-378CIP5.ST25.txt

Met Tyr Arg Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln  
 380 385 390

gtt caa tcc gtg aaa ata agc tgc tta taactaggaa tggtcactgg 1313  
 Val Gln Ser Val Lys Ile Ser Cys Leu  
 395 400

gctgttttctt ca 1325

<210> 123  
 <211> 401  
 <212> PRT  
 <213> Mus musculus

<220>  
 <221> misc\_feature  
 <222> (11)..(11)  
 <223> At position 11, R is a purine.  
 <400> 123

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Leu Leu Asp Ile Ile  
 1 5 10 15

Glu Trp Thr Thr Gln Glu Thr Leu Leu Pro Lys Tyr Leu His Tyr Asp  
 20 25 30

Pro Glu Thr Gly His Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr  
 35 40 45

Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro  
 50 55 60

Cys Pro Asp His Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
 65 70 75 80

Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Ser Val Lys Gln Glu  
 85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr  
 100 105 110

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Ser  
 115 120 125

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Lys  
 130 135 140

Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys  
 145 150 155 160

Ile Lys His Thr Asn Cys Ser Thr Phe Gly Leu Leu Leu Ile Gln Lys  
 165 170 175

Gly Asn Ala Thr His Asp Asn Cys Cys Ser Gly Asn Arg Glu Ala Thr  
 180 185 190

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
 195 200 205  
 Phe Ala Val Pro Thr Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val  
 210 215 220  
 Asp Ser Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
 225 230 235 240  
 Lys Arg Arg His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
 245 250 255  
 Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln  
 260 265 270  
 Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Leu Gly His Ser  
 275 280 285  
 Asn Leu Thr Thr Glu Gln Leu Leu Ala Leu Met Glu Ser Leu Pro Gly  
 290 295 300  
 Lys Lys Ile Ser Pro Glu Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys  
 305 310 315 320  
 Ser Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
 325 330 335  
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu  
 340 345 350  
 Lys Thr Ser His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr  
 355 360 365  
 Met Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu  
 370 375 380  
 Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
 385 390 395 400

Leu

<210> 124  
 <211> 1356  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> CDS  
 <222> (95)..(1297)  
 <223>

## A-378CIP5.ST25.txt

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (63)..(63)

&lt;223&gt; At position 63, Y is a pyrimidine.

&lt;400&gt; 124

gtatatataa cgtgatgagc gtacgggtgc ggagacgcac cggcgcgctc gcccagccgc 60

cgyctccaag cccctgaggt ttccggggac caca atg aac aag ttg ctg tgc tgc 115  
 Met Asn Lys Leu Leu Cys Cys  
 1 5

gcg ctc gtg ttt ctg gac atc tcc att aag tgg acc acc cag gaa acg 163  
 Ala Leu Val Phe Leu Asp Ile Ser Ile Lys Trp Thr Thr Gln Glu Thr  
 10 15 20

ttt cct cca aag tac ctt cat tat gac gaa gaa acc tct cat cag ctg 211  
 Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu  
 25 30 35

ttg tgt gac aaa tgt cct cct ggt acc tac cta aaa caa cac tgt aca 259  
 Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr  
 40 45 50 55

gca aag tgg aag tcc gtg tgc gcc cct tgc cct gac cac tac tac aca 307  
 Ala Lys Trp Lys Ser Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr  
 60 65 70

gac agc tgg cac acc agt gac gag tgt cta tac tgc agc ccc gtg tgc 355  
 Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys  
 75 80 85

aag gag ctg cag tac gtc aag cag gag tgc aat cgc acc cac aac cgc 403  
 Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg  
 90 95 100

gtg tgc gaa tgc aag gaa ggg cgc tac ctt gag ata gag ttc tgc ttg 451  
 Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu  
 105 110 115

aaa cat agg agc tgc cct cct gga ttt gga gtg gtg caa gct gga acc 499  
 Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr  
 120 125 130 135

cca gag cga aat aca gtt tgc aaa aga tgt cca gat ggg ttc ttc tca 547  
 Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser  
 140 145 150

aat gag acg tca tct aaa gca ccc tgt aga aaa cac aca aat tgc agt 595  
 Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser  
 155 160 165

gtc ttt ggt ctc ctg cta act cag aaa gga aat gca aca cac gac aac 643  
 Val Phe Gly Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn  
 170 175 180

ata tgt tcc gga aac agt gaa tca act caa aaa tgt gga ata gat gtt 691  
 Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val  
 185 190 195

acc ctg tgt gag gag gca ttc ttc agg ttt gct gtt cct aca aag ttt 739  
 Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe  
 200 205 210 215

acg cct aac tgg ctt agt gtc ttg gta gac aat ttg cct ggc acc aaa 787  
 Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys  
 Page 31

## A-378CIP5.ST25.txt

220	225	230	
gta aac gca gag agt gta gag agg	ata aaa cgg caa cac agc tca caa	835	
Val Asn Ala Glu Ser Val Glu Arg	Ile Lys Arg Gln His Ser Ser Gln		
235	240 245		
gaa cag act ttc cag ctg ctg aag tta tgg aaa cat caa aac aaa gcc	883		
Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Ala			
250 255 260			
caa gat ata gtc aag aag atc atc caa gat att gac ctc tgt gaa aac	931		
Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn			
265 270 275			
agc gtg cag cgg cac att gga cat gct aac ctc acc ttc gag cag ctt	979		
Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu			
280 285 290 295			
cgt agc ttg atg gaa agc tta ccg gga aag aaa gtg gga gca gaa gac	1027		
Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp			
300 305 310			
att gaa aaa aca ata aag gca tgc aaa ccc agt gac cag atc ctg aag	1075		
Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys			
315 320 325			
ctg ctc agt ttg tgg cga ata aaa aat ggc gac caa gac acc ttg aag	1123		
Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys			
330 335 340			
ggc cta atg cac gca cta aag cac tca aag acg tac cac ttt ccc aaa	1171		
Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys			
345 350 355			
act gtc act cag agt cta aag aag acc atc agg ttc ctt cac agc ttc	1219		
Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe			
360 365 370 375			
aca atg tac aaa ttg tat cag aag tta ttt tta gaa atg ata ggt aac	1267		
Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn			
380 385 390			
cag gtc caa tca gta aaa ata agc tgc tta taactggaaa tggccattga	1317		
Gln Val Gln Ser Val Lys Ile Ser Cys Leu			
395 400			
gctgtttcct cacaattggc gagatcccat ggatgataa			1356
<210> 125			
<211> 401			
<212> PRT			
<213> Homo sapiens			
<220>			
<221> misc_feature			
<222> (63)..(63)			
<223> At position 63, Y is a pyrimidine.			
<400> 125			
Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile			
1 5 10 15			
Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp			
20 25 30			



A-378CIP5.ST25.txt

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
35 40 45

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Ser Val Cys Ala Pro  
50 55 60

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
65 70 75 80

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
100 105 110

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
115 120 125

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
130 135 140

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
145 150 155 160

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
165 170 175

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr  
180 185 190

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
195 200 205

Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val  
210 215 220

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
225 230 235 240

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
245 250 255

Trp Lys His Gln Asn Lys Ala Gln Asp Ile Val Lys Lys Ile Ile Gln  
260 265 270

Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala  
275 280 285

Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly  
290 295 300

A-378CIP5.ST25.txt

Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys  
305 310 315 320

Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
325 330 335

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser  
340 345 350

Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr  
355 360 365

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu  
370 375 380

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
385 390 395 400

Leu

<210> 126  
<211> 139  
<212> PRT  
<213> Homo sapiens

<400> 126

Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys  
1 5 10 15

Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro  
20 25 30

Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala  
35 40 45

Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys  
50 55 60

Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr  
65 70 75 80

Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn  
85 90 95

Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His  
100 105 110

Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly  
115 120 125

Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys  
 130 135

<210> 127  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> huOPG

<400> 127  
 acctacttct ttgaagagta gtcgacgaca cactatttac aggcggcc

48

<210> 128  
 <211> 219  
 <212> PRT  
 <213> Rattus rattus

<400> 128

Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala  
 1 5 10 15

Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser  
 20 25 30

Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn  
 35 40 45

Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro  
 50 55 60

Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro  
 65 70 75 80

Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His  
 85 90 95

Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly  
 100 105 110

Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg  
 115 120 125

Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp  
 130 135 140

Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr  
 145 150 155 160

Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp  
 165 170 175

Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg  
 Page 35

180

185

190

Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly  
 195 200 205

Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr  
 210 215

<210> 129

<211> 281

<212> PRT

<213> Rattus rattus

<400> 129

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu  
 1 5 10 15

Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro  
 20 25 30

His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys  
 35 40 45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
 50 55 60

Gly Thr Tyr Leu Thr Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr  
 65 70 75 80

Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His  
 85 90 95

Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln  
 100 105 110

Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys  
 115 120 125

Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys  
 130 135 140

Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln  
 145 150 155 160

Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg  
 165 170 175

Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys  
 180 185 190

Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp  
 195 200 205

A-378CIP5.ST25.txt

Ser Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys  
210 215 220

Leu Leu Ser Leu Leu Phe Ile Gly Leu Met Thr Arg Thr Gln Arg Trp  
225 230 235 240

Lys Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys  
245 250 255

Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro  
260 265 270

Ser Phe Ser Pro Thr Pro Gly Phe Thr  
275 280

<210> 130  
<211> 207  
<212> PRT  
<213> Rattus rattus

<400> 130

Met Leu Arg Leu Ile Ala Leu Leu Val Cys Val Val Tyr Val Tyr Gly  
1 5 10 15

Asp Asp Val Pro Tyr Ser Ser Asn Gln Gly Lys Cys Gly Gly His Asp  
20 25 30

Tyr Glu Lys Asp Gly Leu Cys Cys Ala Ser Cys His Pro Gly Phe Tyr  
35 40 45

Ala Ser Arg Leu Cys Gly Pro Gly Ser Asn Thr Val Cys Ser Pro Cys  
50 55 60

Glu Asp Gly Thr Phe Thr Ala Ser Thr Asn His Ala Pro Ala Cys Val  
65 70 75 80

Ser Cys Arg Gly Pro Cys Thr Gly His Leu Ser Glu Ser Gln Pro Cys  
85 90 95

Asp Arg Thr His Asp Arg Val Cys Asn Cys Ser Thr Gly Asn Tyr Cys  
100 105 110

Leu Leu Lys Gly Gln Asn Gly Cys Arg Ile Cys Ala Pro Gln Thr Lys  
115 120 125

Cys Pro Ala Gly Tyr Gly Val Ser Gly His Thr Arg Ala Gly Asp Thr  
130 135 140

Leu Cys Glu Lys Cys Pro Pro His Thr Tyr Ser Asp Ser Leu Ser Pro  
145 150 155 160

A-378CIP5.ST25.txt

Thr Glu Arg Cys Gly Thr Ser Phe Asn Tyr Ile Ser Val Gly Phe Asn  
165 170 175

Leu Tyr Pro Val Asn Glu Thr Ser Cys Thr Thr Thr Ala Gly His Asn  
180 185 190

Glu Val Ile Lys Thr Lys Glu Phe Thr Val Thr Leu Asn Tyr Thr  
195 200 205

<210> 131  
<211> 227  
<212> PRT  
<213> Rattus rattus

<400> 131

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu  
1 5 10 15

Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr  
20 25 30

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Thr Thr Asp Gln  
35 40 45

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys  
50 55 60

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp  
65 70 75 80

Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys  
85 90 95

Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg  
100 105 110

Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu  
115 120 125

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg  
130 135 140

Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val  
145 150 155 160

Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr  
165 170 175

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly  
180 185 190

Asn Ala Ser Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser  
 195 200 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser  
 210 215 220

Gln His Thr  
 225

<210> 132  
 <211> 197  
 <212> PRT  
 <213> Rattus rattus

<400> 132

Met Val Ser Leu Pro Arg Leu Cys Ala Leu Trp Gly Cys Leu Leu Thr  
 1 5 10 15

Ala Val His Leu Gly Gln Cys Val Thr Cys Ser Asp Lys Gln Tyr Leu  
 20 25 30

His Asp Gly Gln Cys Cys Asp Leu Cys Gln Pro Gly Ser Arg Leu Thr  
 35 40 45

Ser His Cys Thr Ala Leu Glu Lys Thr Gln Cys His Pro Cys Asp Ser  
 50 55 60

Gly Glu Phe Ser Ala Gln Trp Asn Arg Glu Ile Arg Cys His Gln His  
 65 70 75 80

Arg His Cys Glu Pro Asn Gln Gly Leu Arg Val Lys Lys Glu Gly Thr  
 85 90 95

Ala Glu Ser Asp Thr Val Cys Thr Cys Lys Glu Gly Gln His Cys Thr  
 100 105 110

Ser Lys Asp Cys Glu Ala Cys Ala Gln His Thr Pro Cys Ile Pro Gly  
 115 120 125

Phe Gly Val Met Glu Met Ala Thr Glu Thr Thr Asp Thr Val Cys His  
 130 135 140

Pro Cys Pro Val Gly Phe Phe Ser Asn Gln Ser Ser Leu Phe Glu Lys  
 145 150 155 160

Cys Tyr Pro Trp Thr Ser Cys Glu Asp Lys Asn Leu Glu Val Leu Gln  
 165 170 175

Lys Gly Thr Ser Gln Thr Asn Val Ile Cys Gly Leu Lys Ser Arg Met  
 180 185 190

Arg Ala Leu Leu Val

195

<210> 133  
 <211> 208  
 <212> PRT  
 <213> Rattus rattus

<400> 133

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile Ile  
 1 5 10 15

Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 20 25 30

Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr  
 35 40 45

Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro  
 50 55 60

Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
 65 70 75 80

Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln Glu  
 85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr  
 100 105 110

Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Leu  
 115 120 125

Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
 130 135 140

Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys  
 145 150 155 160

Arg Lys His Thr Asn Cys Ser Ser Leu Gly Leu Leu Leu Ile Gln Lys  
 165 170 175

Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr  
 180 185 190

Gln Asn Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
 195 200 205

<210> 134  
 <211> 224  
 <212> PRT  
 <213> Rattus rattus

<400> 134



Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu  
 1 5 10 15  
 Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys  
 20 25 30  
 Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn  
 35 40 45  
 Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys  
 50 55 60  
 Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr  
 65 70 75 80  
 Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser  
 85 90 95  
 Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly  
 100 105 110  
 Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys  
 115 120 125  
 Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr  
 130 135 140  
 Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His  
 145 150 155 160  
 Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln  
 165 170 175  
 Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro  
 180 185 190  
 Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr  
 195 200 205  
 Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile  
 210 215 220  
 <210> 135  
 <211> 205  
 <212> PRT  
 <213> Rattus rattus  
 <400> 135  
 Met Tyr Val Trp Val Gln Gln Pro Thr Ala Phe Leu Leu Leu Gly Leu  
 1 5 10 15

Ser Leu Gly Val Thr Val Lys Leu Asn Cys Val Lys Asp Thr Tyr Pro  
20 25 30

Ser Gly His Lys Cys Cys Arg Glu Cys Gln Pro Gly His Gly Met Val  
35 40 45

Ser Arg Cys Asp His Thr Arg Asp Thr Val Cys His Pro Cys Glu Pro  
50 55 60

Gly Phe Tyr Asn Glu Ala Val Asn Tyr Asp Thr Cys Lys Gln Cys Thr  
65 70 75 80

Gln Cys Asn His Arg Ser Gly Ser Glu Leu Lys Gln Asn Cys Thr Pro  
85 90 95

Thr Glu Asp Thr Val Cys Gln Cys Arg Pro Gly Thr Gln Pro Arg Gln  
100 105 110

Asp Ser Ser His Lys Leu Gly Val Asp Cys Val Pro Cys Pro Pro Gly  
115 120 125

His Phe Ser Pro Gly Ser Asn Gln Ala Cys Lys Pro Trp Thr Asn Cys  
130 135 140

Thr Leu Ser Gly Lys Gln Ile Arg His Pro Ala Ser Asn Ser Leu Asp  
145 150 155 160

Thr Val Cys Glu Asp Arg Ser Leu Leu Ala Thr Leu Leu Trp Glu Thr  
165 170 175

Gln Arg Thr Thr Phe Arg Pro Thr Thr Val Pro Ser Thr Thr Val Trp  
180 185 190

Pro Arg Thr Ser Gln Leu Pro Ser Thr Pro Thr Leu Val  
195 200 205

<210> 136  
<211> 191  
<212> PRT  
<213> Rattus rattus

<400> 136

Met Gly Asn Asn Cys Tyr Asn Val Val Val Ile Val Leu Leu Leu Val  
1 5 10 15

Gly Cys Glu Lys Val Gly Ala Val Gln Asn Ser Cys Asp Asn Cys Gln  
20 25 30

Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys Ser Cys Pro  
35 40 45

Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn Cys Asn Ile Cys  
Page 42

50

55

60

Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr  
65 70 75 80

His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro  
85 90 95

Gln Cys Thr Arg Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr  
100 105 110

Lys Gln Gly Cys Lys Thr Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn  
115 120 125

Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Arg  
130 135 140

Ser Val Leu Lys Thr Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro  
145 150 155 160

Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu  
165 170 175

Gly Gly Pro Gly Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu  
180 185 190

<210> 137  
<211> 54  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> huOPG

<400> 137  
tatggatgaa gaaacttctc atcagctgct gtgtgataaa tgtccgccgg gtac

54

<210> 138  
<211> 284  
<212> PRT  
<213> Mus musculus

<400> 138

Cys Leu Lys His Arg Ser Cys Pro Pro Gly Ser Gly Val Val Gln Ala  
1 5 10 15

Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Lys Cys Pro Asp Gly Phe  
20 25 30

Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys Ile Lys His Thr Asn  
35 40 45

Cys Ser Thr Phe Gly Leu Leu Leu Ile Gln Lys Gly Asn Ala Thr His  
50 55 60

Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr Gln Lys Cys Gly Ile  
65 70 75 80

Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr  
85 90 95

Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val Asp Ser Leu Pro Gly  
100 105 110

Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Arg His Ser  
115 120 125

Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn  
130 135 140

Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln Asp Ile Ala Leu Cys  
145 150 155 160

Glu Ser Ser Val Gln Arg His Leu Gly His Ser Asn Leu Thr Thr Glu  
165 170 175

Gln Leu Leu Ala Leu Met Glu Ser Leu Pro Gly Lys Lys Ile Ser Pro  
180 185 190

Glu Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys Ser Ser Glu Gln Leu  
195 200 205

Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr  
210 215 220

Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu Lys Thr Ser His Phe  
225 230 235 240

Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr Met Arg Phe Leu His  
245 250 255

Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile  
260 265 270

Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu  
275 280

<210> 139  
<211> 380  
<212> PRT  
<213> Homo sapiens

<400> 139

Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His  
1 5 10 15

## A-378CIP5.ST25.txt

Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His  
 20 25 30  
 Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr  
 35 40 45  
 Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro  
 50 55 60  
 Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His  
 65 70 75 80  
 Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe  
 85 90 95  
 Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala  
 100 105 110  
 Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe  
 115 120 125  
 Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn  
 130 135 140  
 Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His  
 145 150 155 160  
 Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile  
 165 170 175  
 Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr  
 180 185 190  
 Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly  
 195 200 205  
 Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser  
 210 215 220  
 Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn  
 225 230 235 240  
 Lys Ala Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys  
 245 250 255  
 Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu  
 260 265 270  
 Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala  
 275 280 285

A-378CIP5.ST25.txt

Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile  
290 295 300

Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr  
305 310 315 320

Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Lys His Phe  
325 330 335

Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His  
340 345 350

Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile  
355 360 365

Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu  
370 375 380

<210> 140  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> huOPG

<400> 140  
tggaccaccc agaagtacct tcattatgac

30

<210> 141  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> huOPG

<400> 141  
gtcataatga aggtacttct ggggtggtcca

30

<210> 142  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> huOPG

<400> 142  
ggaccacca gcttcattat gacgaagaaa c

31

<210> 143  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> huOPG

<400> 143  
gtttcttctgt cataatgaag ctgggtggtc c 31

<210> 144  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> huOPG

<400> 144  
gtggaccacc caggacgaag aaacctctc 29

<210> 145  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> huOPG

<400> 145  
gagaggtttc ttcgtcctgg gtggtccac 29

<210> 146  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> huOPG

<220>  
<221> misc\_feature  
<223> PCR primer for mutant analogue.

<400> 146  
cgtttcctcc aaagttcctt cattatgac 29

<210> 147  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> huOPG

<400> 147  
gtcataatga aggaactttg gaggaaacg 29

<210> 148  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> huOPG

<400> 148  
ggaaacgttt cctgcaaagt accttcatta tg 32

<210> 149  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> huOPG

<400> 149  
cataatgaag gtactttgca ggaaacgttt cc

32

<210> 150  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> muOPG

<400> 150  
cacgcaaaag tcgggaatag atgtcac

27

<210> 151  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> muOPG

<400> 151  
gtgacatcta ttccccgactt ttgcgtg

27

<210> 152  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> muOPG

<400> 152  
caccctgtcg gaagaggcct tcttc

25

<210> 153  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> muOPG

<400> 153  
gaagaaggcc tcttcgcaca ggggtg

25

<210> 154  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>



<223> muOPG  
 <400> 154  
 tgacctctcg gaaagcagcg tgca 24  
 <210> 155  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> muOPG  
 <400> 155  
 tgcacgctgc tttccgagag gtca 24  
 <210> 156  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> muOPG  
 <400> 156  
 cctcgaaatc gagecgagcag ctcc 24  
 <210> 157  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> muOPG  
 <400> 157  
 cgatttcgag gtctttctcg ttctc 25  
 <210> 158  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> muOPG  
 <400> 158  
 ccgtgaaaat aagctcgta taactaggaa tgg 33  
 <210> 159  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> muOPG  
 <400> 159  
 ccattcctag ttataacgag cttattttca cgg 33  
 <210> 160  
 <211> 38

<212> DNA  
<213> Artificial Sequence

<220>  
<223> muOPG

<400> 160  
cctctgagct caagcttccg aggaccacaa tgaacaag

38

<210> 161  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> muOPG

<400> 161  
cctctctcga gtcaggtgac atctattcca cacttttgcg tggc

44

<210> 162  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> muOPG

<400> 162  
cctctgagct caagcttccg aggaccacaa tgaacaag

38

<210> 163  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer for deletion mutant

<400> 163  
cctctctcga gtcaaggaac agcaaactg aagaaggc

38

<210> 164  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> muOPG

<400> 164  
cctctgagct caagcttccg aggaccacaa tgaacaag

38

<210> 165  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> muOPG

<400> 165  
cctctctcga gtcactctgt ggtgaggttc gagtggcc

38

<210> 166  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> muOPG

<400> 166  
cctctgagct caagcttccg aggaccacaa tgaacaag

38

<210> 167  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> muOPG

<400> 167  
cctctctcga gtcaggatgt tttcaagtgc ttgagggc

38

<210> 168  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> pAMG22

<400> 168

Met Lys His His His His His His Ala Ser Val Asn Ala Leu Glu  
1 5 10 15